

Troponinindikatoren PCT.ST25
SEQUENCE LISTING

<110> Max-Planck-Gesellschaft

<120> Novel genetically encoded bioindicators of calcium-ions

<130> G62276PC

<150> EP 03016691.2

<151> 2003-08-04

<160> 42

<170> PatentIn version 3.1

<210> 1

<211> 1863

<212> DNA

<213> Artificial Sequence

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<223> Calcium binding moiety: cSTnC 15-163

<400> 1

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| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccgga ccacatgaag | 240 |
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| gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac | 600 |
| tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc | 660 |
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<210> 2

<211> 620

<212> PRT

<213> Artificial sequence

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<223> Calcium binding moiety: csTnC 15-163

<400> 2

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
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 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
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 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
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 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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 Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
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 Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
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 Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
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 Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
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<210> 3
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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
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<210> 5

<211> 1863

<212> DNA

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<223> Calcium binding moiety: csTnC 15-163

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| gacggcgacg taaacggcca caagttcagc gtgtccggcg agggcgaggg cgatgccacc | 1260 |
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<223> Calcium binding moiety: csTnC 15-163

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 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
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Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
 225 230 235 240
 Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
 245 250 255
 Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
 260 265 270
 Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
 275 280 285
 Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
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 Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
 305 310 315 320
 Ile Phe Ala Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
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 Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
 340 345 350
 Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
 355 360 365
 Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
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 Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 385 390 395 400
 Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 405 410 415
 Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 420 425 430
 Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
 435 440 445
 Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
 450 455 460

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Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
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Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
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Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
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Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
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Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
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Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
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Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
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Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
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| cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg | 360 |

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ctgaagttca tctgcaccac cggcaagctg cccgtgccct ggcccaccct cgtgaccacc 1380
ttcggctacg gcctgatgtg cttcgccgc taccgacc acatgcgcca gcacgacttc 1440
ttcaagtccg ccatgcccga aggtacgtc caggagcgca ccattctt caaggacgac 1500
ggcaactaca agaccgcgc cgaggtgaag ttcgagggcg acaccctggt gaaccgcatc 1560
gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacia gctggagtac 1620
aactacaaca gccacaacgt ctatatcatg gccgacaagc agaagaacgg catcaaggcc 1680
aacttcaaga tccgccacia catcgaggac ggacgcgtgc agctcgccga ccactaccag 1740
cagaacaccc ccacggcgca cggccccgtg ctgctgcccg acaaccacta cctgagctac 1800
cagtcgccc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc 1860
gtgaccgccg ccgggatcac tctcgcatg gacgagctgt acaagtaa 1908

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<210> 8

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnC

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<400> 8

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
 225 230 235 240

Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
 245 250 255

Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys
 260 265 270

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Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
 275 280 285
 Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
 290 295 300
 Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
 305 310 315 320
 Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
 325 330 335
 Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
 340 345 350
 Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
 355 360 365
 Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
 370 375 380
 Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser Lys
 385 390 395 400
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 405 410 415
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 420 425 430
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 435 440 445
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly
 450 455 460
 Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe
 465 470 475 480
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 485 490 495
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 500 505 510
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 515 520 525
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 530 535 540

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His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 545 550 555 560

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 565 570 575

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 580 585 590

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
 595 600 605

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 610 615 620

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 625 630 635

<210> 9

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: cSTnC EF-hand 2, 51-91

<400> 9

| | |
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| atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac | 60 |
| ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac | 120 |
| ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc | 180 |
| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag | 240 |
| cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg | 360 |
| gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac | 420 |
| aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac | 480 |
| ggcatcaagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc | 540 |
| gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac | 600 |
| tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc | 660 |
| ctgctggagt tcgtgaccgc cgcccgcgtg ctaggccaga accccaccaa agaggagctg | 720 |
| gatgccatca tcgaggaggt ggacgaggat ggcagcggca ccatcgactt cgaggagttc | 780 |
| ctggtgatga tgggtgcgcca gatgaaagag gacgccgagc tcatggtgag caagggcgag | 840 |

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gagctgttca ccggggtggt gcccacctctg gtcgagctgg acggcgacgt aaacggccac 900
 aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaag 960
 ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccttcggc 1020
 tacggcctga tgtgcttcgc ccgctacccc gaccacatgc gccagcacga cttcttcaag 1080
 tccgccatgc ccgaaggcta cgtccaggag cgcacctatct tcttcaagga cgacggcaac 1140
 tacaagaccc ggcgcgaggt gaagtctgag ggcgacaccc tgggtgaaccg catcgagctg 1200
 aagggcatcg acttcaagga ggacggcaac atcctggggc acaagctgga gtacaactac 1260
 aacagccaca acgtctatat catggccgac aagcagaaga acggcatcaa ggccaacttc 1320
 aagatccgcc acaacatcga ggacggcagc gtgcagctcg ccgaccacta ccagcagaac 1380
 acccccatcg gcgacggccc cgtgctgctg cccgacaacc actacctgag ctaccagtcc 1440
 gccctgagca aagaccccaa cgagaagcgc gatcacatgg tcctgctgga gttcgtgacc 1500
 gccgccggga tcactctcgg catggacgag ctgtacaagt aa 1542

<210> 10

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: cTnC EF-hand 2, 51-91

<400> 10

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu
 225 230 235 240
 Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp
 245 250 255
 Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala
 260 265 270
 Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 275 280 285
 Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 290 295 300
 Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 305 310 315 320
 Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 325 330 335
 Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 340 345 350
 Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 355 360 365
 Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 370 375 380

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Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 385 390 395 400

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 405 410 415

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 420 425 430

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 435 440 445

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 450 455 460

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 465 470 475 480

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 485 490 495

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 500 505 510

Lys

<210> 11

<211> 2469

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnC - Gly-Gly - csTnI

<400> 11

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| atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac | 60 |
| ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac | 120 |
| ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc | 180 |
| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag | 240 |
| cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg | 360 |
| gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac | 420 |
| aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac | 480 |

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| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| ggcatcaagg | cccacttcaa | gatccgccac | aacatcgagg | acggcagcgt | gcagctcgcc | 540 |
| gaccactacc | agcagaacac | ccccatcggc | gacggccccg | tgctgctgcc | cgacaaccac | 600 |
| tacctgagca | cccagtccgc | cctgagcaaa | gaccccaacg | agaagcgcg | tcacatgggtc | 660 |
| ctgctggagt | tcgtgaccgc | cgcccgcgtg | ctaattggcgt | caatgacgga | ccagcaggcg | 720 |
| gaggccccgc | ccttcctcag | cgaggagatg | attgctgagt | tcaaagctgc | ctttgacatg | 780 |
| tttgatgcgg | acggtggtgg | ggacatcagc | accaaggagt | tgggcacggt | gatgaggatg | 840 |
| ctggggcaga | acccaccaa | agaggagctg | gatgccatca | tcgaggaggt | ggacgaggat | 900 |
| ggcagcgcca | ccatcgactt | cgaggagttc | ctggtgatga | tggtgcgcca | gatgaaagag | 960 |
| gacgccaagg | gcaagtctga | ggaggagctg | gccaactgct | tccgcattct | cgacaagaac | 1020 |
| gctgatgggt | tcatcgacat | cgaggagctg | ggtgagattc | tcagggccac | tggggagcac | 1080 |
| gtcatcgagg | aggacataga | agacctcatg | aaggattcag | acaagaacaa | tgacggccgc | 1140 |
| attgacttcg | atgagttcct | gaagatgatg | gaggggtgtg | aggagctcgg | cggcattgtct | 1200 |
| gatgaagaga | aaaagcgtcg | tgagccacc | gcccgtcgtc | agcacctgaa | gagtgtctatg | 1260 |
| ctccagcttg | ctgtcactga | aatagaaaaa | gaagcagctg | ctaaagaagt | ggaaaagcaa | 1320 |
| aactacctgg | cagagcatag | ccctcctctg | tccctcccag | ggtccatgca | ggaacttcag | 1380 |
| gaactgagca | aaaaacttca | tgccaagata | gactcagtgg | atgaggaaag | gtatgacaca | 1440 |
| gaggtgaagc | tacagaagac | taacaaggag | ctggaggacc | tgagccagaa | gctgtttgac | 1500 |
| ctgaggggca | agttcaagag | gccacctctg | cgccgggtgc | gcatgtctgc | tgatgccatg | 1560 |
| ctgcgtgccc | tgctgggctc | caagcacaag | gtcaacatgg | acctccgggc | caacctgaag | 1620 |
| caagtcaaga | aggaggacac | ggagaaggag | aaggacctcc | gcgatgtggg | tgactggagg | 1680 |
| aagaacattg | aggagaaatc | tggcatggag | ggcaggaaga | agatgtttga | ggccggcgag | 1740 |
| tccgagctca | tggtgagcaa | gggcgaggag | ctgttcaccg | gggtggtgcc | catcctggtc | 1800 |
| gagctggacg | gcgacgtaaa | cggccacaag | ttcagcgtgt | ccggcgaggg | cgagggcgat | 1860 |
| gccacctacg | gcaagctgac | cctgaagttc | atctgcacca | ccggcaagct | gcccgtgccc | 1920 |
| tggcccaccc | tcgtgaccac | cttcggctac | ggcctgatgt | gcttcgcccg | ctaccccgac | 1980 |
| cacatgcgcc | agcacgactt | cttcaagtcc | gccatgcccg | aaggctacgt | ccaggagcgc | 2040 |
| accatcttct | tcaaggacga | cggcaactac | aagaccgcg | ccgaggtgaa | gttcgagggc | 2100 |
| gacaccctgg | tgaaccgcat | cgagctgaag | ggcatcgact | tcaaggagga | cggcaacatc | 2160 |
| ctggggcaca | agctggagta | caactacaac | agccacaacg | tctatatcat | ggccgacaag | 2220 |
| cagaagaacg | gcataaggc | caacttcaag | atccgccaca | acatcgagga | cggcagcgtg | 2280 |
| cagctcgccg | accactacca | gcagaacacc | cccatcggcg | acggccccgt | gctgctgccc | 2340 |
| gacaaccact | acctgagcta | ccagtccgcc | ctgagcaaa | accccaacga | gaagcgcgat | 2400 |
| cacatggtcc | tgctggagtt | cgtgaccgcc | gccgggatca | ctctcggcat | ggacgagctg | 2460 |
| tacaagtaa | | | | | | 2469 |

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<210> 12

<211> 822

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: cSTnC - Gly-Gly - cSTnI

<400> 12

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
 225 230 235 240
 Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
 245 250 255
 Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys
 260 265 270
 Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
 275 280 285
 Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
 290 295 300
 Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
 305 310 315 320
 Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
 325 330 335
 Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
 340 345 350
 Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
 355 360 365
 Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
 370 375 380
 Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Gly Gly Met Ser
 385 390 395 400
 Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln His Leu
 405 410 415
 Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys Glu Ala
 420 425 430
 Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His Ser Pro
 435 440 445
 Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu Ser Lys
 450 455 460
 Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr Asp Thr
 465 470 475 480

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Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu Ser Gln
 485 490 495
 Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg
 500 505 510
 Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys
 515 520 525
 His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val Lys Lys
 530 535 540
 Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp Trp Arg
 545 550 555 560
 Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys Met Phe
 565 570 575
 Glu Ala Gly Glu Ser Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe
 580 585 590
 Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
 595 600 605
 His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
 610 615 620
 Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
 625 630 635 640
 Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala
 645 650 655
 Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys Ser Ala Met
 660 665 670
 Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
 675 680 685
 Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
 690 695 700
 Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
 705 710 715 720
 Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
 725 730 735
 Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg
 740 745 750

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His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
 755 760 765

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
 770 775 780

Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 785 790 795 800

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly
 805 810 815

Met Asp Glu Leu Tyr Lys
 820

<210> 13

<211> 1959

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 116-135 - Gly-Gly - csTnC

<400> 13

| | |
|--|-----|
| atgggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac | 60 |
| ggcgagctaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac | 120 |
| ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc | 180 |
| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag | 240 |
| cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg | 360 |
| gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac | 420 |
| aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac | 480 |
| ggcatcaagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc | 540 |
| gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac | 600 |
| tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc | 660 |
| ctgctggagt tcgtgaccgc cgcccgcgtg ctcgctgatg ccatgctgcg tgccctgctg | 720 |
| ggctccaagc acaaggtaa cggcggcgcg tcaatgacgg accagcaggc ggaggccccg | 780 |
| gccttctcta gcgaggagat gattgctgag ttcaaagctg cctttgacat gtttgatgcg | 840 |
| gacggtggtg gggacatcag caccaaggag ttgggcacgg tgatgaggat gctgggccag | 900 |
| aacccacca aagaggagct ggatgccatc atcgaggagg tggacgagga tggcagcggc | 960 |

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accatcgact tcgaggagtt cctggtgatg atggtgcgcc agatgaaaga ggacgccaag 1020
 ggcaagtctg aggaggagct ggccaactgc ttccgcatct tcgacaagaa cgctgatggg 1080
 ttcacgcaca tcgaggagct ggggtgagatt ctgagggcca ctggggagca cgtcatcgag 1140
 gaggacatag aagacctcat gaaggattca gacaagaaca atgacggccg cattgacttc 1200
 gatgagttcc tgaagatgat ggaggggtgtg caggagctca tgggtgagcaa gggcgaggag 1260
 ctgttcaccg ggggtggtgcc catcctggtc gagctggacg gcgacgtaaa cggccacaag 1320
 ttcagcgtgt ccggcgaggg cgagggcgat gccacctacg gcaagctgac cctgaagttc 1380
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 ggctgatgt gcttcgcccg ctaccccgac cacatgcgcc agcacgactt cttcaagtcc 1500
 gccatgcccg aaggctacgt ccaggagcgc accatcttct tcaaggacga cggcaactac 1560
 aagaccgcg ccgaggtgaa gttcgagggc gacaccctgg tgaaccgat cgagctgaag 1620
 ggcacgcact tcaaggagga cggcaacatc ctggggcaca agctggagta caactacaac 1680
 agccacaacg tctatatcat ggccgacaag cagaagaacg gcatcaaggc caacttcaag 1740
 atccgccaca acatcgagga cggcagcgtg cagctcgccg accactacca gcagaacacc 1800
 cccatcggcg acggccccgt gctgctgccc gacaaccact acctgagcta ccagtccgcc 1860
 ctgagcaaag accccaacga gaagcgcgat cacatggtcc tgctggagtt cgtgaccgcc 1920
 gccgggatca ctctcgcat ggacgagctg tacaagtaa 1959

<210> 14

<211> 652

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: cSTnI 116-135 - Gly-Gly - cSTnC

<400> 14

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Troponinindikatoren PCT.ST25

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ala Asp Ala Met Leu Arg Ala Leu Leu
225 230 235 240

Gly Ser Lys His Lys Val Asn Gly Gly Ala Ser Met Thr Asp Gln Gln
245 250 255

Ala Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
260 265 270

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
275 280 285

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
290 295 300

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
305 310 315 320

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
325 330 335

Troponinindikatoren PCT.ST25

Glu Asp Ala Lys Gly Lys Ser Glu Glu Leu Ala Asn Cys Phe Arg
 340 345 350
 Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
 355 360 365
 Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
 370 375 380
 Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
 385 390 395 400
 Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
 405 410 415
 Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 420 425 430
 Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 435 440 445
 Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 450 455 460
 Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
 465 470 475 480
 Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
 485 490 495
 Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 500 505 510
 Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 515 520 525
 Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 530 535 540
 Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 545 550 555 560
 Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 565 570 575
 Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 580 585 590
 Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 595 600 605

Troponinindikatoren PCT.ST25

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
610 615 620

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
625 630 635 640

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
645 650

- <210> 15
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 95-131 - Gly-Ser-Gly - csTnC 1-91

<400> 15
atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480
ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600
tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc 660
ctgctggagt tcgtgaccgc cgcccgcgtg ctagacctga gccagaagct gtttgacctg 720
aggggcaagt tcaagaggcc acctctgcgc cggtgctgca tgtctgctga tgccatgctg 780
cgtgccctgc tgggctccaa gcacaaggct ggcagcggca gcatgctaag ggcgtcaatg 840
acggaccagc aggcggaggc ccgcgccctc ctacgcgagg agatgattgc tgagttcaaa 900
gctgcctttg acatgtttga tgcggacggt ggtggggaca tcagcaccaa ggagttgggc 960
acggtgatga ggatgctggg ccagaacccc accaaagagg agctggatgc catcatcgag 1020
gaggtggacg aggatggcag cggcaccatc gacttcgagg agttcctggt gatgatggtg 1080
cgccagatga aagaggacgc cgagctcatg gtgagcaagg gcgaggagct gttcaccggg 1140
gtggtgcccc tcctggctga gctggacggc gacgtaaagc gccacaagtt cagcgtgtcc 1200
ggcgagggcg agggcgatgc cacctacggc aagctgacct tgaagttcat ctgcaccacc 1260

Troponinindikatoren PCT.ST25

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ggcaagctgc ccgtgccctg gcccaccctc gtgaccacct tcggctacgg cctgatgtgc 1320
ttcggccgct accccgacca catgcgccag cactgttct tcaagtccgc catgcccga 1380
ggctacgtcc aggagcgac catcttcttc aaggacgac gcaactacaa gaccgcgcc 1440
gaggtgaagt tcgagggcga caccctggtg aaccgcatcg agctgaaggg catcgacttc 1500
aaggaggacg gcaacatcct ggggcacaag ctggagtaca actacaacag ccacaacgtc 1560
tatatcatgg ccgacaagca gaagaacggc atcaaggcca acttcaagat ccgccacaac 1620
atcgaggacg gcagcgtgca gctcgccgac cactaccagc agaacacccc catcggcgac 1680
ggccccgtgc tgctgccga caaccactac ctgagctacc agtccgccct gagcaaagac 1740
cccaacgaga agcgcgatca catggtcctg ctggagtctg tgaccgccgc cgggatcact 1800
ctcggcatgg acgagctgta caagtaa 1827

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<210> 16

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 95-131 - Gly-Ser-Gly - csTnC 1-91

<400> 16

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1      5      10      15

```

```

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20      25      30

```

```

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35      40      45

```

```

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50      55      60

```

```

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65      70      75      80

```

```

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85      90      95

```

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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100     105     110

```

```

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115     120     125

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Troponinindikatoren PCT.ST25

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Asp Leu Ser Gln Lys Leu Phe Asp Leu
 225 230 235 240

Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg Val Arg Met Ser Ala
 245 250 255

Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys His Lys Val Gly Ser
 260 265 270

Gly Ser Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg
 275 280 285

Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp
 290 295 300

Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly
 305 310 315 320

Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp
 325 330 335

Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe
 340 345 350

Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Glu
 355 360 365

Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 370 375 380

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 385 390 395 400

Troponinindikatoren PCT.ST25

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 405 410 415

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 420 425 430

Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met
 435 440 445

Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 450 455 460

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 465 470 475 480

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 485 490 495

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 500 505 510

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 515 520 525

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 530 535 540

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 545 550 555 560

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 565 570 575

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 580 585 590

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 595 600 605

<210> 17

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 12-161

Troponinindikatoren PCT.ST25

<400> 17

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| atggtgagca agggcgagga gctgttcacc ggggtggtgc ccacctcgtt cgagctggac | 60 |
| ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac | 120 |
| ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc | 180 |
| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag | 240 |
| cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg | 360 |
| gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac | 420 |
| aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac | 480 |
| ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc | 540 |
| gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac | 600 |
| tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc | 660 |
| ctgctggagt tcgtgaccgc cgcccgcatg ctgctgacag aagagcagaa aaatgagttc | 720 |
| aaggcagcct tcgacatctt cgtgctgggc gctgaggatg gctgcatcag caccaaggag | 780 |
| ctgggcaagg tgatgaggat gctggggcag aacccccacc ctgaggagct gcaggagatg | 840 |
| atcgatgagg tggacgagga cggcagcggc acggtggact ttgatgagtt cctgggtcatg | 900 |
| atggttcggt gcatgaagga cgacagcaaa gggaaatctg aggaggagct gtctgacctc | 960 |
| ttccgcatgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg | 1020 |
| ctgcaggcta caggcgagac catcacggag gacgacatcg aggaactcat gaaggacgga | 1080 |
| gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaaggggtgtg | 1140 |
| gaggagctca tggtagcaaa gggcgaggag ctgttcaccg ggggtggtgcc catcctggtc | 1200 |
| gagctggacg gcgacgtaaa cggccacaag ttcagcgtgt ccggcgaggg cgagggcgat | 1260 |
| gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct gcccgtgccc | 1320 |
| tgggccaccc tcgtgaccac cttcggctac ggcctgatgt gcttcgcccg ctaccccgac | 1380 |
| cacatgcgcc agcacgactt cttcaagtcc gccatgcccg aaggctacgt ccaggagcgc | 1440 |
| accatcttct tcaaggacga cggcaactac aagaccgcg ccgaggtgaa gttcgagggc | 1500 |
| gacaccctgg tgaaccgcat cgagctgaag ggcacgact tcaaggagga cggcaacatc | 1560 |
| ctggggcaca agctggagta caactacaac agccacaacg tctatatcat ggccgacaag | 1620 |
| cagaagaacg gcatcaaggc caacttcaag atccgccaca acatcgagga cggcagcgtg | 1680 |
| cagctcgccg accactacca gcagaacacc cccatcggcg acggccccgt gctgctgccc | 1740 |
| gacaaccact acctgagcta ccagtcgcc ctgagcaaag accccaacga gaagcgcgat | 1800 |
| cacatggtcc tgctggagtt cgtgaccgcc gccgggatca ctctcggcat ggacgagctg | 1860 |
| tacaagtaa | 1869 |

<210> 18

Troponinindikatoren PCT.ST25

<211> 622

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: csTnI 12-161

<400> 18

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Troponinindikatoren PCT.ST25

Val Thr Ala Ala Arg Met Leu Leu Thr Glu Glu Gln Lys Asn Glu Phe
225 230 235 240

Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile
245 250 255

Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro
260 265 270

Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly
275 280 285

Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met Met Val Arg Cys
290 295 300

Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu
305 310 315 320

Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu
325 330 335

Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp
340 345 350

Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile
355 360 365

Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met
370 375 380

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
385 390 395 400

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
405 410 415

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
420 425 430

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
435 440 445

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln
450 455 460

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
465 470 475 480

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
485 490 495

Troponinindikatoren PCT.ST25

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
500 505 510

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
515 520 525

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
530 535 540

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
545 550 555 560

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
565 570 575

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser
580 585 590

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
595 600 605

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
610 615 620

<210> 19

<211> 486

<212> DNA

<213> Homo sapiens

<400> 19

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|--|-----|
| atggatgaca tctacaaggc tgcggtagag cagctgacag aagagcagaa aaatgagttc | 60 |
| aaggcagcct tcgacatctt cgtgctgggc gctgaggatg gctgcatcag caccaaggag | 120 |
| ctgggcaagg tgatgaggat gctgggccag aacccaccc ctgaggagct gcaggagatg | 180 |
| atcgatgagg tggacgagga cggcagcggc acggtggact ttgatgagtt cctgggtcatg | 240 |
| atggttcggt gcatgaagga cgacagcaaa gggaaatctg aggaggagct gtctgacctc | 300 |
| ttccgcatgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg | 360 |
| ctgcaggcta caggcgagac catcacggag gacgacatcg aggagctcat gaaggacgga | 420 |
| gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaaggggtgtg | 480 |
| gagtag | 486 |

<210> 20

<211> 161

Troponinindikatoren PCT.ST25

<212> PRT

<213> Homo sapiens

<400> 20

Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln
 1 5 10 15

Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu
 20 25 30

Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu
 35 40 45

Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val
 50 55 60

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met
 65 70 75 80

Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu
 85 90 95

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile
 100 105 110

Asp Leu Asp Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile
 115 120 125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn
 130 135 140

Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val
 145 150 155 160

Glu

<210> 21

<211> 633

<212> DNA

<213> Homo sapiens

<400> 21

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cgccgctcct ccaactaccg cgcttatgcc acggagccgc acgccaagaa aaaatctaag 120

atctccgcct cgagaaaatt gcagctgaag actctgctgc tgcagattgc aaagcaagag 180

Troponinindikatoren PCT.ST25

ctggagcgag aggcggagga gcggcgcgga gagaaggggc gcgctctgag caccgcgtgc 240
 cagccgctgg agttgaccgg gctgggcttc gcggagctgc aggacttggt cgcacagctc 300
 cacgcccgtg tggacaaggt ggatgaagag agatacgaca tagaggcaaa agtcaccaag 360
 aacatcacgg agattgcaga tctgactcag aagatctttg accttcgagg caagttaaag 420
 cggccaccc tgcggagagt gaggatctct gcagatgccca tgatgcaggc gctgctgggg 480
 gcccgggcta aggagtcctt ggacctgcgg gcccacctca agcaggtgaa gaaggaggac 540
 accgagaagg aaaaccggga ggtgggagac tggcggaaga acatcgatgc actgagtgga 600
 atggagggcc gcaagaaaaa gtttgagagc tga 633

<210> 22

<211> 210

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Asp Gly Ser Ser Asp Ala Ala Arg Glu Pro Arg Pro Ala Pro
 1 5 10 15

Ala Pro Ile Arg Arg Arg Ser Ser Asn Tyr Arg Ala Tyr Ala Thr Glu
 20 25 30

Pro His Ala Lys Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln
 35 40 45

Leu Lys Thr Leu Leu Leu Gln Ile Ala Lys Gln Glu Leu Glu Arg Glu
 50 55 60

Ala Glu Glu Arg Arg Gly Glu Lys Gly Arg Ala Leu Ser Thr Arg Cys
 65 70 75 80

Gln Pro Leu Glu Leu Thr Gly Leu Gly Phe Ala Glu Leu Gln Asp Leu
 85 90 95

Cys Arg Gln Leu His Ala Arg Val Asp Lys Val Asp Glu Glu Arg Tyr
 100 105 110

Asp Ile Glu Ala Lys Val Thr Lys Asn Ile Thr Glu Ile Ala Asp Leu
 115 120 125

Thr Gln Lys Ile Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Thr Leu
 130 135 140

Arg Arg Val Arg Ile Ser Ala Asp Ala Met Met Gln Ala Leu Leu Gly
 145 150 155 160

Troponinindikatoren PCT.ST25

Ala Arg Ala Lys Glu Ser Leu Asp Leu Arg Ala His Leu Lys Gln Val
 165 170 175

Lys Lys Glu Asp Thr Glu Lys Glu Asn Arg Glu Val Gly Asp Trp Arg
 180 185 190

Lys Asn Ile Asp Ala Leu Ser Gly Met Glu Gly Arg Lys Lys Lys Phe
 195 200 205

Glu Ser
 210

<210> 23

<211> 483

<212> DNA

<213> Homo sapiens

<400> 23

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 aaggctgcct ttgacatgtt tgatgctgat ggtggtggg acatcagcgt caaggagttg 120
 ggcacggtga tgaggatgct gggccagaca cccaccaagg aggagctgga cgccatcatc 180
 gaggaggtgg atgaggacgg cagcggcacc atcgacttcg aggagttctt ggatcatgatg 240
 gtgcgccaga tgaaagagga cgcgaaaggg aagagcgagg aggagctggc cgagtgccttc 300
 cgcatcttcg acaggaatgc agacggctac atcgaccggg aggagctggc tgagattttc 360
 agggcctccg gggagcacgt gactgacgag gagatcgaat ctctgatgaa agacggcgac 420
 aagaacaacg acggccgcat tgacttcgac gagttcctga agatgatgga gggcgtgcag 480
 taa 483

<210> 24

<211> 160

<212> PRT

<213> Homo sapiens

<400> 24

Met Thr Asp Gln Gln Ala Glu Ala Arg Ser Tyr Leu Ser Glu Glu Met
 1 5 10 15

Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly
 20 25 30

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Gly Asp Ile Ser Val Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly
 35 40 45

Gln Thr Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp
 50 55 60

Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met
 65 70 75 80

Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu
 85 90 95

Ala Glu Cys Phe Arg Ile Phe Asp Arg Asn Ala Asp Gly Tyr Ile Asp
 100 105 110

Pro Glu Glu Leu Ala Glu Ile Phe Arg Ala Ser Gly Glu His Val Thr
 115 120 125

Asp Glu Glu Ile Glu Ser Leu Met Lys Asp Gly Asp Lys Asn Asn Asp
 130 135 140

Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln
 145 150 155 160

<210> 25

<211> 492

<212> DNA

<213> Gallus gallus

<400> 25

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 aaggagttgg gcacggtgat gaggatgctg ggccagaacc ccaccaaaga ggagctggat 180
 gccatcatcg aggaggtgga cgaggatggc agcggcacca tcgacttcga ggagttcctg 240
 gtgatgatgg tgcgccagat gaaagaggac gccaagggca agtctgagga ggagctggcc 300
 aactgcttcc gcatcttcga caagaacgct gatgggttca tcgacatcga ggagctgggt 360
 gagattctca gggccactgg ggagcacgtc atcgaggagg acatagaaga cctcatgaag 420
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 ggtgtgcagt aa 492

<210> 26

<211> 163

<212> PRT

Troponinindikatoren PCT.ST25

<213> Gallus gallus

<400> 26

Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg Ala Phe Leu Ser
 1 5 10 15

Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala
 20 25 30

Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg
 35 40 45

Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu
 50 55 60

Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu
 65 70 75 80

Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu
 85 90 95

Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly
 100 105 110

Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu
 115 120 125

His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp Ser Asp Lys
 130 135 140

Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu
 145 150 155 160

Gly Val Gln

<210> 27

<211> 552

<212> DNA

<213> Gallus gallus

<400> 27

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aagcaaaact acctggcaga gcattgccct cctctgtccc tcccaggatc catgcaggaa 180

cttcaggaac tgtgcaaaaa gcttcattgcc aagatagact cagtggatga ggaaaggat 240

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gacacagagg tgaagctaca gaagactaac aaggagctgg aggacctgag ccagaagctg 300
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 gccatgctgc gtgccctgct gggctccaag cacaagggtca acatggacct ccgggccaac 420
 ctgaagcaag tcaagaagga ggacacggag aaggagaagg acctccgcga tgtgggtgac 480
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<210> 28

<211> 183

<212> PRT

<213> Gallus gallus

<400> 28

Met Ser Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln
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His Leu Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys
 20 25 30

Glu Ala Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His
 35 40 45

Cys Pro Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu
 50 55 60

Cys Lys Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr
 65 70 75 80

Asp Thr Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu
 85 90 95

Ser Gln Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu
 100 105 110

Arg Arg Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly
 115 120 125

Ser Lys His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val
 130 135 140

Lys Lys Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp
 145 150 155 160

Trp Arg Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys
 165 170 175

Troponinindikatoren PCT.ST25

Met Phe Glu Ala Gly Glu Ser
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<210> 29

<211> 486

<212> DNA

<213> Gallus gallus

<400> 29

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ctggggaagg tgatgaggat gctggggcag aacccacccc ctgaggagct gcaggagatg      180
attgatgagg tggatgagga tggcagtggc actgtggact ttgatgagtt ccttgttatg      240
atggttcggt gtatgaaaga tgacagcaaa ggaaaaactg aagaggagct ctcatatctc      300
ttcaggatgt ttgataagaa tgctgatggc tacatcgatc ttgaggaact gaagatcatg      360
ctacaggcaa ctggagagac gatcactgag gatgacatag aagaactgat gaaagatggg      420
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<210> 30

<211> 161

<212> PRT

<213> Gallus gallus

<400> 30

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Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln
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Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu
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Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu
35     40     45
Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val
50     55     60
Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met
65     70     75     80

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Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Thr Glu Glu Glu
 85 90 95

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile
 100 105 110

Asp Leu Glu Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile
 115 120 125

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn
 130 135 140

Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val
 145 150 155 160

Glu

<210> 31

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: TnC41C

<400> 31

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| ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac | 120 |
| ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc | 180 |
| ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag | 240 |
| cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc | 300 |
| ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg | 360 |
| gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac | 420 |
| aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac | 480 |
| ggcatcaagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc | 540 |
| gacctactac agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac | 600 |
| tacctgagca ccagtcgc cctgagcaaa gaccccaacg agaagcgga tcacatggtc | 660 |
| ctgctggagt tcgtgaccgc cgcccgcatg ctgagcgatg aattgactaa ggagcaaact | 720 |
| gcattactac gtaatgcatt taatgctttt gaccctgaaa aaaatggata tatcaacaca | 780 |
| gctatggtgg gtacgatact tagcatgttg ggtcatcaac ttgatgatgc aactcttgct | 840 |
| gacattatcg ctgaagtcga tgaggatggt tcgggccaac tcgaatttga agaatttacc | 900 |

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 gaagctttcc gcctttacga caaagaagga aatggatata taactactgg tgttcttcgt 1020
 gaaatcctgc gcgaactaga cgataaattg acaaatgacg acctggacat gatgattgag 1080
 gaaattgatt ccgatggatc ggggtactgtt gattttgatg aatttatgga agtaatgacc 1140
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 ctgctgcccc acaaccacta cctgagctac cagtccgcc tgagcaaaga cccaacgag 1800
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 gacgagctgt acaagtaa 1878

<210> 32

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: TnC41C

<400> 32

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Arg Met Leu Ser Asp Glu Leu Thr Lys Glu Gln Thr
 225 230 235 240
 Ala Leu Leu Arg Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly
 245 250 255
 Tyr Ile Asn Thr Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His
 260 265 270
 Gln Leu Asp Asp Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu
 275 280 285
 Asp Gly Ser Gly Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala
 290 295 300
 Arg Phe Leu Val Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys
 305 310 315 320
 Glu Ala Phe Arg Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr
 325 330 335

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Gly Val Leu Arg Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn
 340 345 350

Asp Asp Leu Asp Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly
 355 360 365

Thr Val Asp Phe Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp
 370 375 380

Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 385 390 395 400

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 405 410 415

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 420 425 430

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 435 440 445

Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 450 455 460

Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 465 470 475 480

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 485 490 495

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 500 505 510

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 515 520 525

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 530 535 540

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 545 550 555 560

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 565 570 575

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 580 585 590

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 595 600 605

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Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 610 615 620

Lys
625

<210> 33
 <211> 1866
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Calcium binding moiety: TnC41C 5-154

<400> 33
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 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480
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 tacctgagca ccagtcgc cctgagcaaa gacccaacg agaagcgca tcacatggtc 660
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 acgatactta gcatgttggg tcatcaactt gatgatgcaa ctcttgctga cattatcgct 840
 gaagtcgatg aggatgggtc gggccaaatc gaatttgaag aatttaccac cctggcagcc 900
 cgcttccttg tggagagga cgctgaagct atgatggctg aattgaagga agctttccgc 960
 ctttacgaca aagaaggaaa tggatatata actactggtg ttcttcgtga aatcctgcgc 1020
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 ctggacggcg acgtaaagcg ccacaagttc agcgtgtccg gcgagggcga gggcgatgcc 1260
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 cccaccctcg tgaccacctt cggctacggc ctgatgtgct tcgcccgcta ccccgaccac 1380

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 accctggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg 1560
 gggcacaagc tggagtacaa ctacaacagc cacaacgtct atatcatggc cgacaagcag 1620
 aagaacggca tcaaggccaa cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag 1680
 ctcgccgacc actaccagca gaacaccccc atcgcgacg gccccgtgct gctgccccgac 1740
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 atggctctgc tggagtctgt gaccgccgcc gggatcactc tcggcatgga cgagctgtac 1860
 aagtaa 1866

<210> 34

<211> 621

<212> PRT

<213> Artificial Sequence

<220>

<223> Calcium binding moiety: TnC41C 5-154

<400> 34

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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg
 225 230 235 240

Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr
 245 250 255

Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp
 260 265 270

Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly
 275 280 285

Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val
 290 295 300

Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg
 305 310 315 320

Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg
 325 330 335

Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp
 340 345 350

Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe
 355 360 365

Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp Glu Leu Met Val
 370 375 380

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
 385 390 395 400

Troponinindikatoren PCT.ST25

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
 405 410 415

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
 420 425 430

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly
 435 440 445

Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His
 450 455 460

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
 465 470 475 480

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
 485 490 495

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
 500 505 510

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
 515 520 525

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 530 535 540

Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 545 550 555 560

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 565 570 575

Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys
 580 585 590

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
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Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<210> 35

<211> 465

<212> DNA

<213> Drosophila melanogaster

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60

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 tcgggcca aa tcgaatttga agaatttacc accctggcag cccgcttcct tgtggaagag 240
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 aatggatata taactactgg tgttcttcgt gaaatcctgc gcgaactaga cgataaattg 360
 acaaatgacg acctggacat gatgattgag gaaattgatt ccgatggatc ggggtactgtt 420
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<210> 36

<211> 154

<212> PRT

<213> Drosophila melanogaster

<400> 36

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Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr Ala Met
 20 25 30

Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp Ala Thr
 35 40 45

Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly Gln Ile
 50 55 60

Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val Glu Glu
 65 70 75 80

Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg Leu Tyr
 85 90 95

Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg Glu Ile
 100 105 110

Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp Met Met
 115 120 125

Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe Asp Glu
 130 135 140

Phe Met Glu Val Met Thr Gly Gly Asp Asp
 145 150

Troponinindikatoren PCT.ST25

<210> 37
 <211> 468
 <212> DNA
 <213> Drosophila melanogaster

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 cgtcttatgg gtcagccctt cgacaggcag atccttgacg agctgatgca cgaggtcgat 180
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 aagcagggca atggctacat tcccacctcc tgcctgaagg agatcctcaa ggaactggac 360
 gaccagctga ccgaacagga gctcgacatc atgattgagg aaatcgattc cgacggctct 420
 ggcaccgttg attttgatga attcatggag atgatgactg gcgagtaa 468

<210> 38
 <211> 155
 <212> PRT
 <213> Drosophila melanogaster

<400> 38
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 20 25 30
 Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp
 35 40 45
 Arg Gln Ile Leu Asp Glu Leu Met His Glu Val Asp Glu Asp Lys Ser
 50 55 60
 Gly Arg Leu Glu Phe Glu Glu Phe Val Gln Leu Ala Ala Lys Phe Ile
 65 70 75 80
 Val Glu Glu Asp Asp Glu Ala Met Gln Lys Asp Val Arg Glu Ala Phe
 85 90 95
 Arg Leu Tyr Asp Lys Gln Gly Asn Gly Tyr Ile Pro Thr Ser Cys Leu
 100 105 110

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Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
 115 120 125

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp
 130 135 140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu
 145 150 155

<210> 39

<211> 468

<212> DNA

<213> Drosophila melanogaster

<400> 39
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 aacagcttcg atcaccagaa gactggctcc atccccaccg agatggctcg cgacatcctg 120
 cgcctgatgg gtcagccctt cgacaagaag atcctggagg aactgatcga ggaggtcgat 180
 gaggacaagt ccggtcgctt ggaattcggc gagttcgtcc agctggctgc caagttcatc 240
 gtggaggagg atgcggaggc catgcagaag gagctggccg aggcgttccg tttgtacgat 300
 aagcagggca atggcttcat tcccaccacc tgctgaagg agatcctcaa ggagctggac 360
 gaccagctga ccgaacagga gctggacatt atgatcgagg agatcgattc cgatggctcc 420
 ggtacagtgg atttcgatga attcatggag atgatgactg gcgagtaa 468

<210> 40

<211> 155

<212> PRT

<213> Drosophila melanogaster

<400> 40

Met Ser Ser Val Asp Glu Asp Leu Thr Pro Glu Gln Ile Ala Val Leu
 1 5 10 15

Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro
 20 25 30

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp
 35 40 45

Lys Lys Ile Leu Glu Glu Leu Ile Glu Glu Val Asp Glu Asp Lys Ser
 50 55 60

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Gly Arg Leu Glu Phe Gly Glu Phe Val Gln Leu Ala Ala Lys Phe Ile
 65 70 75 80

Val Glu Glu Asp Ala Glu Ala Met Gln Lys Glu Leu Ala Glu Ala Phe
 85 90 95

Arg Leu Tyr Asp Lys Gln Gly Asn Gly Phe Ile Pro Thr Thr Cys Leu
 100 105 110

Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
 115 120 125

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp
 130 135 140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu
 145 150 155

<210> 41

<211> 1833

<212> DNA

<213> Artificial Sequence

<220>

<223> FRET-pair Cop/Phi; Calcium binding moiety: cSTnC 15-163

<400> 41
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 gagctggtgg gcggcggaga gggcaccccc gagcagggcc gcatgaccaa caagatgaag 120
 agcaccaagg gcgccctgac cttcagcccc tacctgctga gccacgtgat gggctacggc 180
 ttctaccact tcggcaccta cccagcggc tacgagaacc cttcctgca cgccatcaac 240
 aacggcggct acaccaacac ccgcatcgag aagtacgagg acggcggcgt gctgcacgtg 300
 agcttcagct accgctacga ggccggccgc gtgatcggcg acttcaaggt ggtgggcacc 360
 ggcttccccg aggacagcgt gatcttcacc gacaagatca tccgcagcaa cgccaccgtg 420
 gagcacctgc acccatggg cgataacgtg ctggtgggca gcttcgcccg caccttcagc 480
 ctgcgcgacg gcggctacta cagcttcgtg gtggacagcc acatgcactt caagagcgcc 540
 atccacccca gcatcctgca gaacgggggc ccatgttcg cttccgcccg cgtggaggag 600
 ctgcacagca acaccgagct gggcatcgtg gaggaccagc acgccttcaa gaccccgatc 660
 gcattcgccc gcatgctcag cgaggagatg attgctgagt tcaaagctgc ctttgacatg 720
 tttgatgcgg acggtggtgg ggacatcagc accaaggagt tgggcacggt gatgaggatg 780
 ctgggccaga accccaccaa agaggagctg gatgccatca tcgaggaggt ggacgaggat 840
 ggcagcggca ccatcgactt cgaggagttc ctggtgatga tggtgcgcca gatgaaagag 900

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gacgccaagg gcaagtctga ggaggagctg gccaactgct tccgcatctt cgacaagaac 960
 gctgatgggt tcatcgacat cgaggagctg ggtgagattc tcagggccac tggggagcac 1020
 gtcacgagg aggacataga agacctcatg aaggattcag acaagaacaa tgacggccgc 1080
 attgacttcg atgagttcct gaagatgatg gaggggtgctc aggagctcat gtccagcggc 1140
 gccctgctgt tccacggcaa gatccccctac gtggtggaga tggagggcaa tgtggatggc 1200
 cacaccttca gcatccgagg caagggtac ggcgatgcca gcgtgggcaa ggtggatgcc 1260
 cagttcatct gcaccaccgg cgatgtgccc gtgccctgga gcaccctggt gaccaccctg 1320
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 aagacccgcg ccgaggtgac cttcgagaat ggcagcgtgt acaatcgcgt gaagctgaat 1500
 ggccagggct tcaagaagga tggccacgtg ctgggcaaga atctggagtt caatttcacc 1560
 cccactgcc tgtacatctg gggcgatcag gccaatcacg gcctgaagag cgccttcaag 1620
 atctgccacg agatcaccgg cagcaagggc gatttcacg tggccgatca caccagatg 1680
 aataccccca tcggcgggcg ccccgatcac gtgcccagat accaccacat gagctaccac 1740
 gtgaagctga gcaaggatgt gaccgatcac cgcgataata tgagcctgaa ggagaccgtg 1800
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<210> 42

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> FRET-pair Cop/Phi; Calcium binding moiety: cSTnC 15-163

<400> 42

Met Gly Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn
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Gly Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln
 20 25 30

Gly Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe
 35 40 45

Ser Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe
 50 55 60

Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn
 65 70 75 80

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Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly
 85 90 95
 Val Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile
 100 105 110
 Gly Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile
 115 120 125
 Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His
 130 135 140
 Pro Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser
 145 150 155 160
 Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His
 165 170 175
 Phe Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met
 180 185 190
 Phe Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly
 195 200 205
 Ile Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg
 210 215 220
 Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met
 225 230 235 240
 Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr
 245 250 255
 Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala
 260 265 270
 Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu
 275 280 285
 Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly
 290 295 300
 Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn
 305 310 315 320
 Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala
 325 330 335
 Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp
 340 345 350

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Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys
 355 360 365

Met Met Glu Gly Val Gln Glu Leu Met Ser Ser Gly Ala Leu Leu Phe
 370 375 380

His Gly Lys Ile Pro Tyr Val Val Glu Met Glu Gly Asn Val Asp Gly
 385 390 395 400

His Thr Phe Ser Ile Arg Gly Lys Gly Tyr Gly Asp Ala Ser Val Gly
 405 410 415

Lys Val Asp Ala Gln Phe Ile Cys Thr Thr Gly Asp Val Pro Val Pro
 420 425 430

Trp Ser Thr Leu Val Thr Thr Leu Thr Tyr Gly Ala Gln Cys Phe Ala
 435 440 445

Lys Tyr Gly Pro Glu Leu Lys Asp Phe Tyr Lys Ser Cys Met Pro Asp
 450 455 460

Gly Tyr Val Gln Glu Arg Thr Ile Thr Phe Glu Gly Asp Gly Asn Phe
 465 470 475 480

Lys Thr Arg Ala Glu Val Thr Phe Glu Asn Gly Ser Val Tyr Asn Arg
 485 490 495

Val Lys Leu Asn Gly Gln Gly Phe Lys Lys Asp Gly His Val Leu Gly
 500 505 510

Lys Asn Leu Glu Phe Asn Phe Thr Pro His Cys Leu Tyr Ile Trp Gly
 515 520 525

Asp Gln Ala Asn His Gly Leu Lys Ser Ala Phe Lys Ile Cys His Glu
 530 535 540

Ile Thr Gly Ser Lys Gly Asp Phe Ile Val Ala Asp His Thr Gln Met
 545 550 555 560

Asn Thr Pro Ile Gly Gly Gly Pro Val His Val Pro Glu Tyr His His
 565 570 575

Met Ser Tyr His Val Lys Leu Ser Lys Asp Val Thr Asp His Arg Asp
 580 585 590

Asn Met Ser Leu Lys Glu Thr Val Arg Ala Val Asp Cys Arg Lys Thr
 595 600 605

Tyr Leu
 610